ABSTRACT OF THE DISCLOSURE

Disclosed are new methods comprising the use of in situ hybridization to detect abnormal nucleic acid sequence copy numbers in one or more genomes wherein repetitive sequences that bind to multiple loci in a reference chromosome spread are either substantially removed and/or their hybridization signals suppressed. The invention termed Comparative Genomic Hybridization (CGH) provides for methods of determining the relative number of copies of nucleic acid sequences in one or more subject genomes or portions thereof (for example, a tumor cell) as a function of the location of those sequences in a reference genome (for example, a normal human genome). The intensity(ies) of the signals from each labeled subject nucleic acid and/or the differences in the ratios between different signals from the labeled subject nucleic acid sequences are compared to determine the relative copy numbers of the nucleic acid sequences in the one or more subject genomes as a function of position along the reference chromosome spread. Amplifications, duplications and/or deletions in the subject genome(s) can be detected. Also provided is a method of determining the absolute copy numbers of substantially all RNA or DNA sequences in subject cell(s) or cell population(s).